

SEQUENCE LISTING

<110> PUBLIC UNIVERSITY OF NAVARRA
<120> "Method of production of recombinant sucrose
5 synthase, use thereof in the manufacture of kits for
determination of sucrose, production of ADPglucose and
production of transgenic plants whose leaves and
storage organs accumulate high contents of ADPglucose
and starch".
10 <130> PCT-180
<150> ES 200400257
<151> 05.02.04
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<213> *Solanum tuberosum*
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<223> Promoter of the 5' region of SS4
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<223> Promoter of the 3' region of SS4
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<210> 3
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<223> SSX

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aaa cct cat gag ctt ttg gct gag ttc gat gca att cgc caa 168
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ctg aaa tcc act cag gaa gcg att gtt ctg ccc cct tgg gtt 252
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<210> 4

<211> 841

<212> protein

5 <213> *Solanum tuberosum*

<223> SSX fused with a histidine-rich amino acid tail
 deducted after expression of SSX in the pET-28a(+) expression plasmid

10 <400>

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				25				30					35				40		
val	leu	thr	arg	val	his	ser	leu	arg	glu	arg	val	asp	ala	thr	leu	ala	ala	his	arg
				45				50				55					60		
asn	glu	ile	leu	leu	phe	leu	ser	arg	ile	glu	ser	his	gly	lys	gly	ile	leu	lys	pro
				65				70				75					80		
his	glu	leu	leu	ala	glu	phe	asp	ala	ile	arg	gln	asp	asp	lys	asn	lys	leu	asn	glu
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gly ala ser asn gly asn phe val leu glu leu asp phe glu pro phe thr ala ser phe	165	170	175	180
pro lys pro thr leu thr lys ser ile gly asn gly val glu phe leu asn arg his leu	185	190	195	200
ser ala lys met phe his asp lys glu ser met thr pro leu leu glu phe leu arg ala	205	210	215	220
his his tyr lys gly lys thr met met leu asn asp arg ile gln asn ser asn thr leu	225	230	235	240
gln asn val leu arg lys ala glu glu tyr leu ile met leu ser pro asp thr pro tyr	245	250	255	260
phe glu phe glu his lys phe gln glu ile gly leu glu lys gly trp gly asp thr ala	265	270	275	280
glu arg val leu glu met val cys met leu leu asp leu leu glu ala pro asp ser cys	285	290	295	300
thr leu glu lys phe leu gly arg ile pro met val phe asn val val ile leu ser pro	305	310	315	320
his gly tyr phe ala gln glu asn val leu gly tyr pro asp thr gly gly gln val val	325	330	335	340
tyr ile leu asp gln val pro ala leu glu arg glu met leu lys arg ile lys glu gln	345	350	355	360
gly leu asp ile ile pro arg ile leu ile val thr arg leu leu pro asp ala val gly	365	370	375	380
thr thr cys gly gln arg ile glu lys val tyr gly ala glu his ser his ile leu arg	385	390	395	400
val pro phe arg thr glu lys gly ile val arg lys trp ile ser arg phe glu val trp	405	410	415	420
pro tyr met glu thr phe ile glu asp val ala lys glu ile ser ala glu leu gln ala	425	430	435	440
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his lys leu gly val thr gln cys thr ile ala his ala leu glu lys thr lys tyr pro	465	470	475	480
asp ser asp ile tyr trp lys lys phe asp glu lys tyr his phe ser ser gln phe thr	485	490	495	500
ala asp leu ile ala met asn his thr asp phe ile ile thr ser thr phe gln glu ile	505	510	515	520
ala gly ser lys asp thr val gly gln tyr glu ser his met ala phe thr met pro gly	525	530	535	540
leu tyr arg val val his gly ile asn val phe asp pro lys phe asn ile val ser pro	545	550	555	560
gly ala asp ile asn leu tyr phe ser tyr ser glu thr glu lys arg leu thr ala phe	565	570	575	580
his pro glu ile asp glu leu leu tyr ser asp val glu asn asp glu his leu cys val	585	590	595	600
leu lys asp arg thr lys pro ile leu phe thr met ala arg leu asp arg val lys asn	605	610	615	620
leu thr gly leu val glu trp tyr ala lys asn pro arg leu arg gly leu val asn leu	625	630	635	640
val val val gly gly asp arg arg lys glu ser lys asp leu glu glu gln ala glu met	645	650	655	660

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ser gln met asn arg val arg asn gly glu leu tyr arg tyr ile ala asp thr lys gly			
685	690	695	700
ala phe val gln pro ala phe tyr glu ala phe gly leu thr val val glu ala met thr			
705	710	715	720
cys gly leu pro thr phe ala thr asn his gly gly pro ala glu ile ile val his gly			
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lys ser gly phe his ile asp pro tyr his gly glu gln ala ala asp leu leu ala asp			
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phe phe glu lys cys lys lys glu pro ser his trp glu thr ile ser thr gly gly leu			
765	770	775	780
lys arg ile gln glu lys tyr thr trp gln ile tyr ser glu arg leu leu thr leu ala			
785	790	795	800
ala val tyr gly phe trp lys his val ser lys leu asp arg leu glu ile arg arg tyr			
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<211> 41

5 <212> DNA

<213> *Solanum tuberosum*

<220>

<223> "Forward" promoter required for the point
mutagenesis of SSX.

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<212> DNA

25 <213> *Solanum tuberosum*

<220>

<223> "Forward" promoter required for point mutagenesis
of SSX and production of SS5.

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<213> *Solanum tuberosum*

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<213> *Solanum tuberosum*

<220>

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aaa cct cac gag ctt ttg gct gag ttc gat gca att cgc caa 168
gat gac aaa aac aaa ctg aac gaa cat gca ttc gaa gaa ccc 210
ctg aaa tcc act cag gaa gcg att gtt ctg ccc cct tgg gtt 252
gca ctt gct att cgt ttg agg cct ggt gtc tgg gaa tac atc 294
cgt gtg aac gtc aat gca cta gtt gtc gag gag ctg tcc gtc 336
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cgc gct cac cat tat aag ggc aag aca atg atg ctg aat gat 588
agg ata cag aat tcg aat act ctt caa aat gtc cta agg aag 630
gca gag gaa tac ctc att atg ctt tcc cca gat act cca tat 672
ttc gaa ttc gag cac aag ttc caa gaa atc gga ttg gag aag 714
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gcc cac gcg ttg gag aaa acg aag tat cct gat tcc gac att 1344
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<210> 12

5 <211> 841

<212> protein

<213> *Solanum tuberosum*

<223> SS5 fused with a histidine-rich amino acid sequence

<400>

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asn glu ile leu leu phe leu ser arg ile glu ser his gly lys gly ile leu lys pro	65	70	75	80
his glu leu leu ala glu phe asp ala ile arg gln asp asp lys asn lys leu asn glu	85	90	95	100
his ala phe glu glu pro leu lys ser thr gln glu ala ile val leu pro pro trp val	105	110	115	120
ala leu ala ile arg leu arg pro gly val trp glu tyr ile arg val asn val asn ala	125	130	135	140
leu val val glu glu leu ser val pro glu tyr leu gln phe lys glu glu leu val asp	145	150	155	160
gly ala ser asn gly asn phe val leu glu leu asp phe glu pro phe thr ala ser phe	165	170	175	180
pro lys pro thr leu thr lys ser ile gly asn gly val glu phe leu asn arg his leu	185	190	195	200
ser ala lys met phe his asp lys glu ser met thr pro leu leu glu phe leu arg ala	205	210	215	220
his his tyr lys gly lys thr met met leu asn asp arg ile gln asn ser asn thr leu	225	230	235	240
gln asn val leu arg lys ala glu glu tyr leu ile met leu ser pro asp thr pro tyr	245	250	255	260
phe glu phe glu his lys phe gln glu ile gly leu glu lys gly trp gly asp thr ala	265	270	275	280
glu arg val leu glu met val cys met leu leu asp leu leu glu ala pro asp ser cys	285	290	295	300
thr leu glu lys phe leu gly arg ile pro met val phe asn val val ile leu ser pro	305	310	315	320
his gly tyr phe ala gln glu asn val leu gly tyr pro asp thr gly gly gln val val	325	330	335	340
tyr ile leu asp gln val pro ala leu glu arg glu met leu lys arg ile lys glu gln	345	350	355	360
gly leu asp ile ile pro arg ile leu ile val thr arg leu leu pro asp ala val gly	365	370	375	380
thr thr cys gly gln arg ile glu lys val tyr gly ala glu his ser his ile leu arg	385	390	395	400
val pro phe arg thr glu lys gly ile val arg lys trp ile ser arg phe glu val trp	405	410	415	420
pro tyr met glu thr phe ile glu asp val ala lys glu ile ser ala glu leu gln ala	425	430	435	440
lys pro asp leu ile ile gly asn tyr ser glu gly asn leu ala ala ser leu leu ala	445	450	455	460
his lys leu gly val thr gln cys thr ile ala his ala leu glu lys thr lys tyr pro	465	470	475	480
asp ser asp ile tyr trp lys lys phe asp glu lys tyr his phe ser ser gln phe thr	485	490	495	500

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505	510	515	520
ala gly ser lys	asp thr val gly gln tyr glu ser his met ala phe thr met pro gly		
525	530	535	540
leu tyr arg val	val his gly ile asn val phe asp pro lys phe asn ile val ser pro		
545	550	555	560
gly ala asp ile	asn leu tyr phe ser tyr ser glu thr glu lys arg leu thr ala ser		
565	570	575	580
his pro glu ile	asp glu leu leu tyr ser asp val glu asn asp glu his leu cys val		
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leu lys asp arg	thr lys pro ile leu phe thr met ala arg leu asp arg val lys asn		
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785	790	795	800
ala val tyr gly	phe trp lys his val ser lys leu asp arg leu glu ile arg arg tyr		
805	810	815	820
leu glu met phe	tyr ala leu lys tyr arg lys met ala glu ala val pro leu ala ala		
825	830	835	840
glu			
841			